



# SEQUENCE LISTING

## GENERAL INFORMATION

- (i) APPLICANT: Murphy, Patricia  
White, Marga  
Olson, Sheri  
Yoshikawa, Matthew  
Jackson, Geoffrey  
Eskanderi, Tara  
Schryer, Brenda  
Park, Michael
- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES  
OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 133
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
  - (B) STREET: 1800 M St., NW
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/084,471
  - (B) FILING DATE: 22 May 1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/055,784
  - (B) FILING DATE: 15 August 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/064,926
  - (B) FILING DATE: 07 November 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/065,367
  - (B) FILING DATE: 12 November 1997
- (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/071,715
- (B) FILING DATE: 01 May 1998

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Reid G. Adler
- (B) REGISTRATION NUMBER: 30,988
- (C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-467-7000
- (B) TELEFAX: 202-467-7258

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 26...75
- (D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AGGGATTTC TTTGTTTTAT TTTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC 60
AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTA TTCTT 105
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...210
- (D) OTHER INFORMATION: Exon 15\*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT 60
ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT 120
CTGTATCTTG CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC 180
CAAGTTCCTT CTGCGTGTTC TCATAAACAG GTATGTGT 218
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 34...221
- (D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
tttttctttt ttgtgtgtgt ttattttgtg tagctgtata cgtatggcgt ttctaaacat 60
tgcataaaaa ttaacagcaa aaatgcagag tcttttcagt ttcacactga agattatttt 120
ggtaaggaaa gtttatggac tggaaaagga atacagttgg ctgatgggtg atgggtcata 180
ccctccaatg atggaaagc tggaaaagaa gaattttata ggtactctat gcaaaaagat 240
tgtgtgttaa cttttatg                                     258
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGTG GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
                                     Met Pro Ile
                                     1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
  5              10              15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
```

20	25	30	35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA				381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	40	45	50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG				429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	55	60	65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG				477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	70	75	80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT				525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	85	90	95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA				573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	100	105	110	115
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC				621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	120	125	130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA				669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	135	140	145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG ACT				717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	150	155	160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT				765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	165	170	175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA				813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	180	185	190	195
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC				861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	200	205	210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT				909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	215	220	225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT				957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn				

230	235	240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT	GAA AAC ACA AAT CAA AGA	1005	
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser	Glu Asn Thr Asn Gln Arg		
245	255		
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053		
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys			
260	265	270	275
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101		
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu			
280	285	290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149		
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser			
295	300	305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197		
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val			
310	315	320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245		
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp			
325	330	335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293		
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val			
340	345	350	355
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341		
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala			
360	365	370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389		
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val			
375	380	385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437		
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu			
390	395	400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485		
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys			
405	410	415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533		
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg			
420	425	430	435
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581		
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser			

440										445					450					
CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG		1629			
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys					
455					460					465										
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA		1677			
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala					
470					475					480										
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG		1725			
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln					
485					490					495										
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT		1773			
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr					
500					505					510					515					
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA		1821			
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys					
520					525					530										
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA		1869			
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser					
535					540					545										
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG		1917			
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp					
550					555					560										
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA		1965			
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu					
565					570					575										
ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT		2013			
Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His					
580					585					590					595					
GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA		2061			
Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser					
600					605					610										
GAA	CTA	ATT	AAC	TGT	TCA	GCC	CAG	TTT	GAA	GCA	AAT	GCT	TTT	GAA	GCA		2109			
Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	Phe	Glu	Ala					
615					620					625										
CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG		2157			
Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val					
630					635					640										
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA		2205			
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu					

645	650	655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr 660 665 670 675			2253
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala 680 685 690			2301
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp 695 700 705			2349
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser 710 715 720			2397
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His 725 730 735			2445
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser 740 745 750 755			2493
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu 760 765 770			2541
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg 775 780 785			2589
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr 790 795 800			2637
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln 805 810 815			2685
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro 820 825 830 835			2733
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe 840 845 850			2781
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr			2829

855	860	865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe 870 875 880			2877
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895			2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915			2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930			3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945			3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960			3117
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975			3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995			3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010			3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025			3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040			3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055			3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser			3453

1060	1065	1070	1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	1080	1085	1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	1095	1100	1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	1110	1115	1120	3597
CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	1125	1130	1135	3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	1140	1145	1150	3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	1160	1165	1170	3741
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	1175	1180	1185	3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	1190	1195	1200	3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	1205	1210	1215	3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	1220	1225	1230	3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	1240	1245	1250	3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	1255	1260	1265	4029
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val				4077

1270	1275	1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285	1290	1295	4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300	1305	1310 1315	4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320	1325	1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335	1340	1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350	1355	1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365	1370	1375	4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380	1385	1390 1395	4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400	1405	1410	4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415	1420	1425	4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430	1435	1440	4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445	1450	1455	4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460	1465	1470 1475	4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu			4701

1480	1485	1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495	1500	1505	4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510	1515	1520	4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525	1530	1535	4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540	1545	1550	4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560	1565	1570	4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575	1580	1585	4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590	1595	1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605	1610	1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620	1625	1630	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640	1645	1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655	1660	1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670	1675	1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp			5325

1685	1690	1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GCA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700	1705	1710	5373 1715
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720	1725	1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735	1740	1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750	1755	1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765	1770	1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780	1785	1790	5613 1795
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800	1805	1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815	1820	1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830	1835	1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845	1850	1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860	1865	1870	5853 1875
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880	1885	1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser			5949

1895	1900	1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920			5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935			6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955			6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970			6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985			6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000			6237
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015			6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035			6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050			6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065			6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080			6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095			6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu			6573

2100	2105	2110	2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	2120	2125	2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	2135	2140	2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	2150	2155	2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	2165	2170	2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	2180	2185	2190	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	2200	2205	2210	6861
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	2215	2220	2225	6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	2230	2235	2240	6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	2245	2250	2255	7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	2260	2265	2270	7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	2280	2285	2290	7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	2295	2300	2305	7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His				7197

2310	2315	2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325	2330	2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340	2345	2350 2355	7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360	2365	2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375	2380	2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390	2395	2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405	2410	2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420	2425	2430 2435	7533
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440	2445	2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2455	2460	2465	7629
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470	2475	2480	7677
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485	2490	2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500	2505	2510 2515	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val			7821

2520	2525	2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG	TAT ACG TAT GGC GTT TCT AAA		7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys			
2535	2540	2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC			7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His			
2550	2555	2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA			7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile			
2565	2570	2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT			8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala			
2580	2585	2590	2595
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT			8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp			
2600	2605	2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC			8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile			
2615	2620	2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT			8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala			
2630	2635	2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA			8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg			
2645	2650	2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA			8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile			
2660	2665	2670	2675
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT			8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser			
2680	2685	2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA			8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys			
2695	2700	2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT			8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp			
2710	2715	2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC			8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val			

2725	2730	2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA			8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly			
2740	2745	2750	2755
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA			8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro			
2760	2765	2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC			8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg			
2775	2780	2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG			8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu			
2790	2795	2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT			8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp			
2805	2810	2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA			8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser			
2820	2825	2830	2835
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA			8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala			
2840	2845	2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT			8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr			
2855	2860	2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA			8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro			
2870	2875	2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA			8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln			
2885	2890	2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT			8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala			
2900	2905	2910	2915
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT			9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn			
2920	2925	2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA			9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu			

2935	2940	2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950	2955	2960	9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965	2970	2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980	2985	2990	9213
2995			
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000	3005	3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015	3020	3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030	3035	3040	9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045	3050	3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060	3065	3070	9453
3075			
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080	3085	3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095	3100	3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110	3115	3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125	3130	3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe			9693

3140	3145	3150	3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	3160	3165	3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	3175	3180	3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	3190	3195	3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	3205	3210	3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	3220	3225	3230	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	3240	3245	3250	9981
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	3255	3260	3265	10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val	3270	3275	3280	10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	3285	3290	3295	10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	3300	3305	3310	10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	3320	3325	3330	10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	3335	3340	3345	10269
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile				10317

3350	3355	3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT			10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr			
3365	3370	3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG			10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu			
3380	3385	3390	3395
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA			10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr			
3400	3405	3410	
ATT ACA ACT AAA AAA TAT ATC TAA			10485
Ile Thr Thr Lys Lys Tyr Ile			
3415			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55					60					
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70				75					80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90					95		
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
		100					105					110			
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115					120					125				
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130				135					140					
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145				150					155					160	



Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	580	585	590
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	595	600	605
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	610	615	620
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	625	630	635
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	645	650	655
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	660	665	670
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	675	680	685
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	690	695	700
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	705	710	715
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	725	730	735
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	740	745	750
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	755	760	765
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	770	775	780
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	785	790	795
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	805	810	815
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	820	825	830
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	835	840	845
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	850	855	860
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	865	870	875
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	885	890	895
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	900	905	910
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	915	920	925
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	930	935	940
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	945	950	955
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	965	970	975
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	980	985	990

Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser  
 995 1000 1005  
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile  
 1010 1015 1020  
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr  
 1025 1030 1035 104  
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln  
 1045 1050 1055  
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu  
 1060 1065 1070  
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro  
 1075 1080 1085  
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr  
 1090 1095 1100  
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu  
 1105 1110 1115 112  
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile  
 1125 1130 1135  
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu  
 1140 1145 1150  
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met  
 1155 1160 1165  
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly  
 1170 1175 1180  
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys  
 1185 1190 1195 120  
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe  
 1205 1210 1215  
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu  
 1220 1225 1230  
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser  
 1235 1240 1245  
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys  
 1250 1255 1260  
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp  
 1265 1270 1275 128  
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn  
 1285 1290 1295  
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn  
 1300 1305 1310  
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser  
 1315 1320 1325  
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn  
 1330 1335 1340  
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp  
 1345 1350 1355 136  
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly  
 1365 1370 1375  
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val  
 1380 1385 1390  
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln  
 1395 1400 1405

Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser  
 1410 1415 1420  
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys  
 1425 1430 1435 144  
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu  
 1445 1450 1455  
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys  
 1460 1465 1470  
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His  
 1475 1480 1485  
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val  
 1490 1495 1500  
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr  
 1505 1510 1515 152  
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys  
 1525 1530 1535  
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly  
 1540 1545 1550  
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys  
 1555 1560 1565  
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu  
 1570 1575 1580  
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn  
 1585 1590 1595 160  
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu  
 1605 1610 1615  
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser  
 1620 1625 1630  
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala  
 1635 1640 1645  
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile  
 1650 1655 1660  
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser  
 1665 1670 1675 168  
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly  
 1685 1690 1695  
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly  
 1700 1705 1710  
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp  
 1715 1720 1725  
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser  
 1730 1735 1740  
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser  
 1745 1750 1755 176  
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu  
 1765 1770 1775  
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser  
 1780 1785 1790  
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile  
 1795 1800 1805  
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn  
 1810 1815 1820

Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly  
 1825 1830 1835 184  
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His  
 1845 1850 1855  
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys  
 1860 1865 1870  
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys  
 1875 1880 1885  
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu  
 1890 1895 1900  
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val  
 1905 1910 1915 192  
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met  
 1925 1930 1935  
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu  
 1940 1945 1950  
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser  
 1955 1960 1965  
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys  
 1970 1975 1980  
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe  
 1985 1990 1995 200  
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe  
 2005 2010 2015  
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala  
 2020 2025 2030  
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn  
 2035 2040 2045  
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys  
 2050 2055 2060  
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu  
 2065 2070 2075 208  
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro  
 2085 2090 2095  
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg  
 2100 2105 2110  
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys  
 2115 2120 2125  
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu  
 2130 2135 2140  
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln  
 2145 2150 2155 216  
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn  
 2165 2170 2175  
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met  
 2180 2185 2190  
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn  
 2195 2200 2205  
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu  
 2210 2215 2220  
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu  
 2225 2230 2235 224

Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys  
 2245 2250 2255  
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg  
 2260 2265 2270  
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn  
 2275 2280 2285  
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu  
 2290 2295 2300  
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu  
 2305 2310 2315 232  
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg  
 2325 2330 2335  
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro  
 2340 2345 2350  
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu  
 2355 2360 2365  
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln  
 2370 2375 2380  
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly  
 2385 2390 2395 240  
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe  
 2405 2410 2415  
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg  
 2420 2425 2430  
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys  
 2435 2440 2445  
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln  
 2450 2455 2460  
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu  
 2465 2470 2475 248  
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys  
 2485 2490 2495  
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu  
 2500 2505 2510  
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly  
 2515 2520 2525  
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly  
 2530 2535 2540  
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe  
 2545 2550 2555 256  
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly  
 2565 2570 2575  
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp  
 2580 2585 2590  
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro  
 2595 2600 2605  
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr  
 2610 2615 2620  
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys  
 2625 2630 2635 264  
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu  
 2645 2650 2655

Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile  
 2660 2665 2670  
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu  
 2675 2680 2685  
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser  
 2690 2695 2700  
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu  
 2705 2710 2715 272  
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu  
 2725 2730 2735  
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile  
 2740 2745 2750  
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu  
 2755 2760 2765  
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg  
 2770 2775 2780  
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro  
 2785 2790 2795 280  
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly  
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 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu  
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 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala  
 2850 2855 2860  
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr  
 2865 2870 2875 288  
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg  
 2885 2890 2895  
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala  
 2900 2905 2910  
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala  
 2915 2920 2925  
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile  
 2930 2935 2940  
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln  
 2945 2950 2955 296  
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser  
 2965 2970 2975  
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro  
 2980 2985 2990  
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile  
 2995 3000 3005  
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn  
 3010 3015 3020  
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val  
 3025 3030 3035 304  
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His  
 3045 3050 3055  
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val  
 3060 3065 3070

Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala  
 3075 3080 3085  
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys  
 3090 3095 3100  
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile  
 3105 3110 3115 312  
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu  
 3125 3130 3135  
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu  
 3140 3145 3150  
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn  
 3155 3160 3165  
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu  
 3170 3175 3180  
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser  
 3185 3190 3195 320  
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu  
 3205 3210 3215  
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu  
 3220 3225 3230  
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met  
 3235 3240 3245  
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn  
 3250 3255 3260  
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro  
 3265 3270 3275 328  
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys  
 3285 3290 3295  
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile  
 3300 3305 3310  
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe  
 3315 3320 3325  
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu  
 3330 3335 3340  
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys  
 3345 3350 3355 336  
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser  
 3365 3370 3375  
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys  
 3380 3385 3390  
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys  
 3395 3400 3405  
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile  
 3410 3415

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 229...10482

(D) OTHER INFORMATION: BRCA2 (OMI2)

(ix) FEATURE:

(A) NAME/KEY: variation

(B) LOCATION: 3624

(D) OTHER INFORMATION: R = A or G. Xaa (amino acid position 1132) = Lys.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC      60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG      120
ACAGATTGTG GACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT      180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT      237
                                         Met Pro Ile
                                         1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC      285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
      5              10              15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT      333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
      20              25              30              35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA      381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
              40              45              50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG      429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
              55              60              65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG      477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
      70              75              80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT      525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
      85              90              95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA      573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
      100              105              110              115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC      621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
              120              125              130
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TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
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TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp 550 555 560	1917
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu 565 570 575	1965
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His 580 585 590 595	2013
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser 600 605 610	2061
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala 615 620 625	2109
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val 630 635 640	2157
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu 645 650 655	2205
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr 660 665 670 675	2253
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala 680 685 690	2301
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp 695 700 705	2349
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser 710 715 720	2397
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His 725 730 735	2445
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser 740 745 750 755	2493

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu 760 765 770	2541
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg 775 780 785	2589
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr 790 795 800	2637
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln 805 810 815	2685
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro 820 825 830 835	2733
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe 840 845 850	2781
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr 855 860 865	2829
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe 870 875 880	2877
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895	2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915	2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930	3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945	3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960	3117

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975	3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995	3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010	3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025	3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040	3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055	3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075	3453
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120	3597
CAG TTT GAA TTT ACT CAG TTT AGA AAR CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys 1125 1130 1135	3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr 1140 1145 1150 1155	3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro 1160 1165 1170	3741

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu 1175 1180 1185	3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser 1190 1195 1200	3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe 1205 1210 1215	3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235	3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250	3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265	4029
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280	4077
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285 1290 1295	4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315	4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375	4365



GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715	5373
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720 1725 1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735 1740 1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1755 1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	5613

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	5661
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	5709
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	5757
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	5805
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	5853
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	5901
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	5949
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	5997
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	6045
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	6093
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	6141
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	6189
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	6237
1990 1995 2000	

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115	6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210	6861

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225	6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240	6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255	7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275	7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290	7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305	7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320	7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355	7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485



ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Lys Glu Ala 2840 2845 2850	8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865	8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880	8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895	8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915	8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930	9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu 2935 2940 2945	9069
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960	9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2985 2990 2995	9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040	9357

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155	9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410	10461
ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415	10485

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: variation

(B) LOCATION: 1132

(D) OTHER INFORMATION: Xaa = Lys (from codon AAR,  
R = A or G).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5				10					15		
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
		20					25					30			
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
	35					40					45				
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55					60					
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65				70					75					80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90						95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
		100						105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115						120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130				135						140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145				150					155					160	
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
			165					170						175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
	180						185						190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
	195						200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
	210			215						220					
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225				230						235				240	
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
			245					250						255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
	260					265						270			
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
	275					280						285			
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
	290				295						300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305				310					315					320	
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
			325					330						335	

Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
	370					375					380				
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
			405					410						415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
	435						440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
	450					455					460				
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
465					470					475					480
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
			485					490						495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
			500					505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
	515					520						525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
	530					535					540				
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
			565					570						575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr
	580						585						590		
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
	595					600						605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
			645					650						655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
		660						665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
	675					680						685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690					695					700				
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710					715					720
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
			725					730					735		
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
			740					745					750		

Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
		755					760					765			
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
	770					775					780				
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly
785				790					795					800	
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu
			805						810					815	
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu
		820						825					830		
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys
		835					840					845			
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln
850						855					860				
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu
865				870						875				880	
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn
			885					890						895	
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr
		900						905					910		
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val
	915						920					925			
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys
930						935					940				
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys
945				950						955				960	
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser
			965					970						975	
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys
		980						985					990		
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser
	995					1000						1005			
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile
1010						1015					1020				
Lys	Lys	Ser	Lys	Met	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	
1025				1030					1035					104	
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln
			1045					1050						1055	
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu
		1060						1065					1070		
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro
	1075						1080					1085			
Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr
1090						1095					1100				
Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu
1105					1110					1115				112	
Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Xaa	Pro	Ser	Tyr	Ile
			1125					1130						1135	
Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu
		1140						1145					1150		
Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met
		1155					1160						1165		

Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	1170	1175	1180
Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	1185	1190	1195
Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	1205	1210	1215
Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	1220	1225	1230
Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser	1235	1240	1245
Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser	Lys	1250	1255	1260
Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His	Asn	Asp	1265	1270	1275
Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	1285	1290	1295
Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	1300	1305	1310
Tyr	Lys	Arg	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	1315	1320	1325
Arg	Asn	Ser	His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn	1330	1335	1340
Asp	Thr	Val	Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp	1345	1350	1355
Gln	His	Asn	Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	1365	1370	1375
Asn	Thr	Gln	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	1380	1385	1390
Ala	Lys	Ala	Gln	Glu	Ala	Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln	1395	1400	1405
Leu	Thr	Ala	Thr	Lys	Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser	1410	1415	1420
Asp	Thr	Phe	Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	1425	1430	1435
Glu	Ser	Phe	Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	1445	1450	1455
Leu	His	Asn	Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys	1460	1465	1470
Asn	Lys	Met	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His	1475	1480	1485
Lys	Ile	Leu	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu	Val	1490	1495	1500
Thr	Phe	Gln	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Pro	Thr	1505	1510	1515
Leu	Leu	Gly	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys	Ile	Ala	Lys	1525	1530	1535
Glu	Ser	Leu	Asp	Lys	Val	Lys	Asn	Leu	Phe	Asp	Glu	Lys	Glu	Gln	Gly	1540	1545	1550
Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp	Ala	Lys	Thr	Leu	Lys	1555	1560	1565
Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Ile	Glu	1570	1575	1580

Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn		
1585	1590	1595 160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu		
	1605	1610 1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser		
	1620	1625 1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala		
	1635	1640 1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile		
	1650	1655 1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser		
1665	1670	1675 168
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly		
	1685	1690 1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly		
	1700	1705 1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp		
	1715	1720 1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser		
	1730	1735 1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser		
1745	1750	1755 176
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu		
	1765	1770 1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser		
	1780	1785 1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile		
	1795	1800 1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
	1810	1815 1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835 184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		
	1845	1850 1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
	1860	1865 1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
	1875	1880 1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
	1890	1895 1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915 192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		
	1925	1930 1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
	1940	1945 1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
	1955	1960 1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
	1970	1975 1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995 200

Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe  
 2005 2010 2015  
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala  
 2020 2025 2030  
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn  
 2035 2040 2045  
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys  
 2050 2055 2060  
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu  
 2065 2070 2075 208  
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro  
 2085 2090 2095  
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg  
 2100 2105 2110  
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys  
 2115 2120 2125  
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu  
 2130 2135 2140  
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln  
 2145 2150 2155 216  
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn  
 2165 2170 2175  
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met  
 2180 2185 2190  
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn  
 2195 2200 2205  
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu  
 2210 2215 2220  
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu  
 2225 2230 2235 224  
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys  
 2245 2250 2255  
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg  
 2260 2265 2270  
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn  
 2275 2280 2285  
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu  
 2290 2295 2300  
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu  
 2305 2310 2315 232  
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg  
 2325 2330 2335  
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro  
 2340 2345 2350  
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu  
 2355 2360 2365  
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln  
 2370 2375 2380  
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly  
 2385 2390 2395 240  
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe  
 2405 2410 2415

His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg	2420	2425	2430
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys	2435	2440	2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln	2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu	2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys	2485	2490	2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu	2500	2505	2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly	2515	2520	2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly	2530	2535	2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe	2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly	2565	2570	2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp	2580	2585	2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro	2595	2600	2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr	2610	2615	2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys	2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu	2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile	2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu	2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser	2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu	2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu	2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile	2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu	2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg	2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro	2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly	2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu	2820	2825	2830

Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala  
 2850 2855 2860  
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr  
 2865 2870 2875 288  
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg  
 2885 2890 2895  
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala  
 2900 2905 2910  
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala  
 2915 2920 2925  
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile  
 2930 2935 2940  
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln  
 2945 2950 2955 296  
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser  
 2965 2970 2975  
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro  
 2980 2985 2990  
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile  
 2995 3000 3005  
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn  
 3010 3015 3020  
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val  
 3025 3030 3035 304  
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His  
 3045 3050 3055  
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val  
 3060 3065 3070  
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala  
 3075 3080 3085  
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys  
 3090 3095 3100  
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile  
 3105 3110 3115 312  
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu  
 3125 3130 3135  
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu  
 3140 3145 3150  
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn  
 3155 3160 3165  
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu  
 3170 3175 3180  
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser  
 3185 3190 3195 320  
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu  
 3205 3210 3215  
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu  
 3220 3225 3230  
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met  
 3235 3240 3245

Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
3250						3255					3260				
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
3265					3270				3275					328	
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys
				3285				3290						3295	
Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
			3300					3305					3310		
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
		3315				3320					3325				
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
3330						3335					3340				
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
3345					3350					3355				336	
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
				3365					3370					3375	
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
			3380					3385					3390		
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
		3395				3400						3405			
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
3410						3415									

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC	CTCGGGTGTC	TTTTGCGGCG	GTGGGTCGCC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTGTG	GACCGGCGCG	GTTTTGTGTC	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA	CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA	ATG CCT ATT	237
				Met Pro Ile		
				1		
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC						285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys						
5		10		15		

AAC	AAA	GCA	GAT	TTA	GGA	CCA	ATA	AGT	CTT	AAT	TGG	TTT	GAA	GAA	CTT	333
Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe	Glu	Glu	Leu	
20					25					30					35	
TCT	TCA	GAA	GCT	CCA	CCC	TAT	AAT	TCT	GAA	CCT	GCA	GAA	GAA	TCT	GAA	381
Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu	Glu	Ser	Glu	
				40					45					50		
CAT	AAA	AAC	AAC	AAT	TAC	GAA	CCA	AAC	CTA	TTT	AAA	ACT	CCA	CAA	AGG	429
His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr	Pro	Gln	Arg	
			55					60					65			
AAA	CCA	TCT	TAT	AAT	CAG	CTG	GCT	TCA	ACT	CCA	ATA	ATA	TTC	AAA	GAG	477
Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	Phe	Lys	Glu	
		70					75					80				
CAA	GGG	CTG	ACT	CTG	CCG	CTG	TAC	CAA	TCT	CCT	GTA	AAA	GAA	TTA	GAT	525
Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	Glu	Leu	Asp	
	85					90					95					
AAA	TTC	AAA	TTA	GAC	TTA	GGA	AGG	AAT	GTT	CCC	AAT	AGT	AGA	CAT	AAA	573
Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	Arg	His	Lys	
100					105					110					115	
AGT	CTT	CGC	ACA	GTG	AAA	ACT	AAA	ATG	GAT	CAA	GCA	GAT	GAT	GTT	TCC	621
Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	Asp	Val	Ser	
				120					125					130		
TGT	CCA	CTT	CTA	AAT	TCT	TGT	CTT	AGT	GAA	AGT	CCT	GTT	GTT	CTA	CAA	669
Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	Val	Leu	Gln	
			135				140						145			
TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT	717
Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	Cys	Gly	Ser	
		150					155					160				
TTG	TTT	CAT	ACA	CCA	AAG	TTT	GTG	AAG	GGT	CGT	CAG	ACA	CCA	AAA	CAT	765
Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	Pro	Lys	His	
	165					170					175					
ATT	TCT	GAA	AGT	CTA	GGA	GCT	GAG	GTG	GAT	CCT	GAT	ATG	TCT	TGG	TCA	813
Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	Ser	Trp	Ser	
180					185					190				195		
AGT	TCT	TTA	GCT	ACA	CCA	CCC	ACC	CTT	AGT	TCT	ACT	GTG	CTC	ATA	GTC	861
Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val	
				200					205				210			
AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT	909
Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala	
			215					220				225				

AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
AAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	

AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	



TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	
1380 1385 1390 1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT	4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	
1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT	4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	
1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT	4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	
1430 1435 1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC	4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	
1445 1450 1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG	4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	
1460 1465 1470 1475	

GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG	4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	
1480 1485 1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG	4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	

CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100 2105 2110 2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621
His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	
2120 2125 2130	
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	
2135 2140 2145	
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA	6717
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	
2150 2155 2160	
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT	6765
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	
2165 2170 2175	
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	
2180 2185 2190 2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	
2200 2205 2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT	7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
2405 2410 2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
2420 2425 2430 2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
2440 2445 2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
2455 2460 2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
2470 2475 2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
2500 2505 2510 2515	

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
2520 2525 2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
2740 2745 2750 2755	
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
2760 2765 2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
2775 2780 2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
2790 2795 2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
2805 2810 2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
2820 2825 2830 2835	
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys	
1 5 10 15	
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe	
20 25 30	
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu	
35 40 45	
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr	
50 55 60	
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile	
65 70 75 80	
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys	
85 90 95	
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser	
100 105 110	
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp	
115 120 125	
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val	
130 135 140	

Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
			180					185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
		195					200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
210					215						220				
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235					240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245					250					255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
			260					265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
		275					280					285			
His	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
		290					295				300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315					320
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325					330					335	
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
370					375					380					
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
				405					410					415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
		435					440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Thr	Val	
450					455						460				
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
465					470					475					480
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
				485					490					495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
			500					505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
			515				520						525		
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
530					535					540					
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560

73

Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys
			980					985					990		
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser
		995					1000					1005			
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile
	1010					1015					1020				
Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr
1025					1030					1035				104	
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln
			1045					1050						1055	
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu
		1060						1065					1070		
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro
	1075						1080					1085			
Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr
1090					1095						1100				
Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu
1105					1110					1115				112	
Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile
			1125					1130						1135	
Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu
		1140						1145					1150		
Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met
		1155					1160					1165			
Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly
	1170					1175					1180				
Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys
1185					1190					1195				120	
Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe
			1205					1210						1215	
Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu
		1220						1225					1230		
Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser
	1235					1240						1245			
Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser	Lys
	1250					1255					1260				
Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His	Asn	Asp
1265					1270					1275				128	
Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn
			1285					1290						1295	
Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn
		1300						1305					1310		
Tyr	Lys	Arg	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser
	1315					1320						1325			
Arg	Asn	Ser	His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn
	1330					1335					1340				
Asp	Thr	Val	Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp
1345					1350					1355				136	
Gln	His	Asn	Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly
			1365					1370					1375		
Asn	Thr	Gln	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val
		1380						1385					1390		

Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln	1395	1400	1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser	1410	1415	1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys	1425	1430	1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu	1445	1450	1455
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys	1460	1465	1470
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His	1475	1480	1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val	1490	1495	1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr	1505	1510	1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys	1525	1530	1535
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly	1540	1545	1550
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys	1555	1560	1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu	1570	1575	1580
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn	1585	1590	1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu	1605	1610	1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser	1620	1625	1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala	1635	1640	1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile	1650	1655	1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser	1665	1670	1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly	1685	1690	1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly	1700	1705	1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp	1715	1720	1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser	1730	1735	1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser	1745	1750	1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu	1765	1770	1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser	1780	1785	1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile	1795	1800	1805

Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
1810	1815	1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		
	1845	1850
		1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
	1860	1865
		1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
	1875	1880
		1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
	1890	1895
		1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		
	1925	1930
		1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
	1940	1945
		1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
	1955	1960
		1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
	1970	1975
		1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995
		200
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe		
	2005	2010
		2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala		
	2020	2025
		2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn		
	2035	2040
		2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys		
	2050	2055
		2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu		
2065	2070	2075
		208
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro		
	2085	2090
		2095
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg		
	2100	2105
		2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys		
	2115	2120
		2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu		
	2130	2135
		2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln		
2145	2150	2155
		216
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn		
	2165	2170
		2175
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met		
	2180	2185
		2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn		
	2195	2200
		2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu		
	2210	2215
		2220

Thr Glu Ala Val	Glu Ile Ala Lys	Ala Phe Met	Glu Asp Asp	Glu Leu
2225	2230	2235		224
Thr Asp Ser Lys	Leu Pro Ser His	Ala Thr His	Ser Leu Phe	Thr Cys
	2245	2250		2255
Pro Glu Asn Glu	Glu Met Val Leu	Ser Asn Ser	Arg Ile Gly	Lys Arg
	2260	2265		2270
Arg Gly Glu Pro	Leu Ile Leu Val	Gly Glu Pro	Ser Ile Lys	Arg Asn
	2275	2280		2285
Leu Leu Asn Glu	Phe Asp Arg Ile	Ile Glu Asn	Gln Glu Lys	Ser Leu
	2290	2295		2300
Lys Ala Ser Lys	Ser Thr Pro Asp	Gly Thr Ile	Lys Asp Arg	Arg Leu
2305	2310	2315		232
Phe Met His His	Val Ser Leu Glu	Pro Ile Thr	Cys Val Pro	Phe Arg
	2325	2330		2335
Thr Thr Lys Glu	Arg Gln Glu Ile	Gln Asn Pro	Asn Phe Thr	Ala Pro
	2340	2345		2350
Gly Gln Glu Phe	Leu Ser Lys Ser	His Leu Tyr	Glu His Leu	Thr Leu
	2355	2360		2365
Glu Lys Ser Ser	Ser Asn Leu Ala	Val Ser Gly	His Pro Phe	Tyr Gln
	2370	2375		2380
Val Ser Ala Thr	Arg Asn Glu Lys	Met Arg His	Leu Ile Thr	Thr Gly
2385	2390	2395		240
Arg Pro Thr Lys	Val Phe Val Pro	Pro Phe Lys	Thr Lys Ser	His Phe
	2405	2410		2415
His Arg Val Glu	Gln Cys Val Arg	Asn Ile Asn	Leu Glu Glu	Asn Arg
	2420	2425		2430
Gln Lys Gln Asn	Ile Asp Gly His	Gly Ser Asp	Asp Ser Lys	Asn Lys
	2435	2440		2445
Ile Asn Asp Asn	Glu Ile His Gln	Phe Asn Lys	Asn Asn Ser	Asn Gln
	2450	2455		2460
Ala Ala Ala Val	Thr Phe Thr Lys	Cys Glu Glu	Glu Pro Leu	Asp Leu
2465	2470	2475		248
Ile Thr Ser Leu	Gln Asn Ala Arg	Asp Ile Gln	Asp Met Arg	Ile Lys
	2485	2490		2495
Lys Lys Gln Arg	Gln Arg Val Phe	Pro Gln Pro	Gly Ser Leu	Tyr Leu
	2500	2505		2510
Ala Lys Thr Ser	Thr Leu Pro Arg	Ile Ser Leu	Lys Ala Ala	Val Gly
	2515	2520		2525
Gly Gln Val Pro	Ser Ala Cys Ser	His Lys Gln	Leu Tyr Thr	Tyr Gly
	2530	2535		2540
Val Ser Lys His	Cys Ile Lys Ile	Asn Ser Lys	Asn Ala Glu	Ser Phe
2545	2550	2555		256
Gln Phe His Thr	Glu Asp Tyr Phe	Gly Lys Glu	Ser Leu Trp	Thr Gly
	2565	2570		2575
Lys Gly Ile Gln	Leu Ala Asp Gly	Gly Trp Leu	Ile Pro Ser	Asn Asp
	2580	2585		2590
Gly Lys Ala Gly	Lys Glu Glu Phe	Tyr Arg Ala	Leu Cys Asp	Thr Pro
	2595	2600		2605
Gly Val Asp Pro	Lys Leu Ile Ser	Arg Ile Trp	Val Tyr Asn	His Tyr
	2610	2615		2620
Arg Trp Ile Ile	Trp Lys Leu Ala	Ala Met Glu	Cys Ala Phe	Pro Lys
2625	2630	2635		264

Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu	2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile	2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu	2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser	2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu	2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu	2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile	2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu	2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg	2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro	2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly	2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu	2820	2825	2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu	2835	2840	2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala	2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr	2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg	2885	2890	2895
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala	2900	2905	2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala	2915	2920	2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile	2930	2935	2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln	2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser	2965	2970	2975
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro	2980	2985	2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile	2995	3000	3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn	3010	3015	3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val	3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His	3045	3050	3055

Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val	3060	3065	3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala	3075	3080	3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys	3090	3095	3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile	3105	3110	3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu	3125	3130	3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu	3140	3145	3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn	3155	3160	3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu	3170	3175	3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser	3185	3190	3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Lys	3205	3210	3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu	3220	3225	3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met	3235	3240	3245
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn	3250	3255	3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro	3265	3270	3275
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys	3285	3290	3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile	3300	3305	3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe	3315	3320	3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu	3330	3335	3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys	3345	3350	3355
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser	3365	3370	3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys	3380	3385	3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys	3395	3400	3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile	3410	3415	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10485 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 229...10482  
(D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asn Gln Ala Asp Asp Val Ser	
120 125 130	

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp 550 555 560	1917
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu 565 570 575	1965
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His 580 585 590 595	2013
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser 600 605 610	2061
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala 615 620 625	2109
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val 630 635 640	2157
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu 645 650 655	2205
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr 660 665 670 675	2253
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala 680 685 690	2301
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp 695 700 705	2349
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser 710 715 720	2397
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His 725 730 735	2445
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser 740 745 750 755	2493

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT	3453
Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser	
1060 1065 1070 1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA	3501
Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	
1080 1085 1090	
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA	3549
Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	
1095 1100 1105	
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597
Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	
1110 1115 1120	
CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG	3645
Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	
1125 1130 1135	
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT	3693
Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	
1140 1145 1150 1155	
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741
Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	

ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	
1380 1385 1390 1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT	4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	
1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT	4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	
1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT	4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	
1430 1435 1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC	4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	
1445 1450 1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG	4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	
1460 1465 1470 1475	
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG	4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	
1480 1485 1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG	4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115	6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210	6861

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT	7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
2405 2410 2415	



ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155	9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410	10461
ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415	10485

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50					55					60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70					75				80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90						95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
			100					105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115						120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130					135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155				160	
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
			165					170					175		
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
		180						185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
	195						200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
210					215					220					
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235				240	
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
			245						250					255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
		260						265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
	275						280				285				
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
	290					295					300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315				320	
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
			325						330					335	
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
		340						345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
	355						360					365			
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser

370	375	380
Lys Glu Val Val Pro Ser	Leu Ala Cys Glu Trp Ser	Gln Leu Thr Leu
385	390	395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile		400
	405	410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu		415
	420	425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg		430
	435	440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val		445
	450	455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys		460
465	470	475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser		480
	485	490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro		495
	500	505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn		510
	515	520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr		525
	530	535
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn		540
545	550	555
Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn		560
	565	570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr		575
	580	585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp		590
	595	600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala		605
	610	615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His		620
625	630	635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr		640
	645	650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg		655
	660	665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr		670
	675	680
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro		685
	690	695
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp		700
705	710	715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala		720
	725	730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp		735
	740	745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr		750
	755	760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met		765
	770	775
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly		780

785		790		795		800
Asn Asn Tyr Glu Ser	Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu					
	805		810		815	
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu						
	820		825		830	
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys						
	835		840		845	
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln						
	850		855		860	
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu						
	865		870		875	880
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn						
	885		890		895	
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr						
	900		905		910	
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val						
	915		920		925	
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys						
	930		935		940	
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys						
	945		950		955	960
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser						
	965		970		975	
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys						
	980		985		990	
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser						
	995		1000		1005	
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile						
	1010		1015		1020	
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr						
	1025		1030		1035	104
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln						
	1045		1050		1055	
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu						
	1060		1065		1070	
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro						
	1075		1080		1085	
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr						
	1090		1095		1100	
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu						
	1105		1110		1115	112
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile						
	1125		1130		1135	
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu						
	1140		1145		1150	
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met						
	1155		1160		1165	
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly						
	1170		1175		1180	
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys						
	1185		1190		1195	120
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe						

	1205	1210	1215
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu			
1220	1225	1230	
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser			
1235	1240	1245	
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys			
1250	1255	1260	
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp			
1265	1270	1275	128
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn			
1285	1290	1295	
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn			
1300	1305	1310	
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser			
1315	1320	1325	
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn			
1330	1335	1340	
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp			
1345	1350	1355	136
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly			
1365	1370	1375	
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val			
1380	1385	1390	
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln			
1395	1400	1405	
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser			
1410	1415	1420	
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys			
1425	1430	1435	144
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu			
1445	1450	1455	
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys			
1460	1465	1470	
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His			
1475	1480	1485	
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val			
1490	1495	1500	
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr			
1505	1510	1515	152
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys			
1525	1530	1535	
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly			
1540	1545	1550	
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys			
1555	1560	1565	
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu			
1570	1575	1580	
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn			
1585	1590	1595	160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu			
1605	1610	1615	
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser			

	1620		1625		1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala					
1635		1640		1645	
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile					
1650	1655		1660		
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser					
1665	1670		1675		168
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly					
1685		1690		1695	
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly					
1700		1705		1710	
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp					
1715	1720		1725		
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser					
1730	1735		1740		
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser					
1745	1750		1755		176
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu					
1765		1770		1775	
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser					
1780		1785		1790	
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile					
1795		1800		1805	
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn					
1810	1815		1820		
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly					
1825	1830		1835		184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His					
1845		1850		1855	
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys					
1860		1865		1870	
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys					
1875		1880		1885	
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu					
1890	1895		1900		
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val					
1905	1910		1915		192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met					
1925		1930		1935	
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu					
1940		1945		1950	
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser					
1955		1960		1965	
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys					
1970		1975		1980	
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe					
1985	1990		1995		200
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe					
2005		2010		2015	
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala					
2020		2025		2030	
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn					

2035					2040					2045						
Val	Val	Asn	Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys	
2050					2055					2060						
Gln	Val	Ser	Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	
2065					2070					2075					208	
Glu	Glu	Phe	Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	
2085					2090					2095						
Thr	Ser	Arg	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	
2100					2105					2110						
Asn	Pro	Glu	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	
2115					2120					2125						
Glu	Phe	Lys	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	
2130					2135					2140						
Asn	Asn	His	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	
2145					2150					2155					216	
Asp	Lys	Gln	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	
2165					2170					2175						
Ile	His	Val	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	
2180					2185					2190						
Glu	Ile	Gly	Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	
2195					2200					2205						
Ile	Glu	Val	Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	
2210					2215					2220						
Thr	Glu	Ala	Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu	
2225					2230					2235					224	
Thr	Asp	Ser	Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys	
2245					2250					2255						
Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg	
2260					2265					2270						
Arg	Gly	Glu	Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn	
2275					2280					2285						
Leu	Leu	Asn	Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu	
2290					2295					2300						
Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Gly	Thr	Ile	Lys	Asp	Arg	Arg	Leu	
2305					2310					2315					232	
Phe	Met	His	His	Val	Ser	Leu	Glu	Pro	Ile	Thr	Cys	Val	Pro	Phe	Arg	
2325					2330					2335						
Thr	Thr	Lys	Glu	Arg	Gln	Glu	Ile	Gln	Asn	Pro	Asn	Phe	Thr	Ala	Pro	
2340					2345					2350						
Gly	Gln	Glu	Phe	Leu	Ser	Lys	Ser	His	Leu	Tyr	Glu	His	Leu	Thr	Leu	
2355					2360					2365						
Glu	Lys	Ser	Ser	Ser	Asn	Leu	Ala	Val	Ser	Gly	His	Pro	Phe	Tyr	Gln	
2370					2375					2380						
Val	Ser	Ala	Thr	Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly	
2385					2390					2395					240	
Arg	Pro	Thr	Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lys	Ser	His	Phe	
2405					2410					2415						
His	Arg	Val	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg	
2420					2425					2430						
Gln	Lys	Gln	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys	
2435					2440					2445						
Ile	Asn	Asp	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn	Gln	

2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu		
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		248
	2485	2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		2495
	2500	2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		2510
	2515	2520
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		2525
	2530	2535
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		2540
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		256
	2565	2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		2575
	2580	2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		2590
	2595	2600
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		2605
	2610	2615
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		2620
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		264
	2645	2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		2655
	2660	2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		2670
	2675	2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		2685
	2690	2695
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		2700
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		272
	2725	2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		2735
	2740	2745
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		2750
	2755	2760
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		2765
	2770	2775
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		2780
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		280
	2805	2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		2815
	2820	2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		2830
	2835	2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		2845
	2850	2855
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		2860

2865	2870	2875	288
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg			
2885	2890	2895	
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala			
2900	2905	2910	
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala			
2915	2920	2925	
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile			
2930	2935	2940	
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln			
2945	2950	2955	296
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser			
2965	2970	2975	
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro			
2980	2985	2990	
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile			
2995	3000	3005	
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn			
3010	3015	3020	
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val			
3025	3030	3035	304
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His			
3045	3050	3055	
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val			
3060	3065	3070	
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala			
3075	3080	3085	
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys			
3090	3095	3100	
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile			
3105	3110	3115	312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu			
3125	3130	3135	
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu			
3140	3145	3150	
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn			
3155	3160	3165	
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu			
3170	3175	3180	
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser			
3185	3190	3195	320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu			
3205	3210	3215	
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu			
3220	3225	3230	
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met			
3235	3240	3245	
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn			
3250	3255	3260	
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro			
3265	3270	3275	328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys			

	3285		3290		3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile					
	3300		3305		3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe					
	3315		3320		3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu					
	3330		3335		3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys					
	3345		3350		3355
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser					
	3365		3370		3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys					
	3380		3385		3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys					
	3395		3400		3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile					
	3410		3415		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
	Met Pro Ile
	1
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381

Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005



Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253



Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA ATA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT	3453
Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser	
1060 1065 1070 1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA	3501

Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	
1080 1085 1090	
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA	3549
Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	
1095 1100 1105	
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597
Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	
1110 1115 1120	
CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG	3645
Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	
1125 1130 1135	
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT	3693
Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	
1140 1145 1150 1155	
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741
Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125

Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	Asn	Ile	Glu	
1285						1290					1295					
ATG	ACT	ACT	GGC	ACT	TTT	GTT	GAA	GAA	ATT	ACT	GAA	AAT	TAC	AAG	AGA	4173
Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	Tyr	Lys	Arg	
1300					1305					1310					1315	
AAT	ACT	GAA	AAT	GAA	GAT	AAC	AAA	TAT	ACT	GCT	GCC	AGT	AGA	AAT	TCT	4221
Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	Arg	Asn	Ser	
				1320					1325					1330		
CAT	AAC	TTA	GAA	TTT	GAT	GGC	AGT	GAT	TCA	AGT	AAA	AAT	GAT	ACT	GTT	4269
His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn	Asp	Thr	Val	
			1335					1340						1345		
TGT	ATT	CAT	AAA	GAT	GAA	ACG	GAC	TTG	CTA	TTT	ACT	GAT	CAG	CAC	AAC	4317
Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp	Gln	His	Asn	
		1350					1355					1360				
ATA	TGT	CTT	AAA	TTA	TCT	GGC	CAG	TTT	ATG	AAG	GAG	GGA	AAC	ACT	CAG	4365
Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	Asn	Thr	Gln	
		1365				1370					1375					
ATT	AAA	GAA	GAT	TTG	TCA	GAT	TTA	ACT	TTT	TTG	GAA	GTT	GCG	AAA	GCT	4413
Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	Ala	Lys	Ala	
1380					1385					1390					1395	
CAA	GAA	GCA	TGT	CAT	GGT	AAT	ACT	TCA	AAT	AAA	GAA	CAG	TTA	ACT	GCT	4461
Gln	Glu	Ala	Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln	Leu	Thr	Ala	
			1400						1405					1410		
ACT	AAA	ACG	GAG	CAA	AAT	ATA	AAA	GAT	TTT	GAG	ACT	TCT	GAT	ACA	TTT	4509
Thr	Lys	Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser	Asp	Thr	Phe	
		1415					1420					1425				
TTT	CAG	ACT	GCA	AGT	GGG	AAA	AAT	ATT	AGT	GTC	GCC	AAA	GAG	TCA	TTT	4557
Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	Glu	Ser	Phe	
	1430					1435					1440					
AAT	AAA	ATT	GTA	AAT	TTC	TTT	GAT	CAG	AAA	CCA	GAA	GAA	TTG	CAT	AAC	4605
Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	Leu	His	Asn	
	1445				1450					1455						
TTT	TCC	TTA	AAT	TCT	GAA	TTA	CAT	TCT	GAC	ATA	AGA	AAG	AAC	AAA	ATG	4653
Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys	Asn	Lys	Met	
1460				1465					1470					1475		
GAC	ATT	CTA	AGT	TAT	GAG	GAA	ACA	GAC	ATA	GTT	AAA	CAC	AAA	ATA	CTG	4701
Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His	Lys	Ile	Leu	
			1480					1485				1490				
AAA	GAA	AGT	GTC	CCA	GTT	GGT	ACT	GGA	AAT	CAA	CTA	GTG	ACC	TTC	CAG	4749

Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373



Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100 2105 2110 2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621

His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	
2120 2125 2130	
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	
2135 2140 2145	
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA	6717
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	
2150 2155 2160	
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT	6765
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	
2165 2170 2175	
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	
2180 2185 2190 2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	
2200 2205 2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245

His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT	7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
2405 2410 2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
2420 2425 2430 2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
2440 2445 2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
2455 2460 2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
2470 2475 2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
2500 2505 2510 2515	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
2520 2525 2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869

Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493



Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741

Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50					55					60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70					75					80
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
				85					90					95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
			100					105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
		115					120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130						135				140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met



595	600	605
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala		
610	615	620
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His		
625	630	635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr		
645	650	655
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg		
660	665	670
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr		
675	680	685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro		
690	695	700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp		
705	710	715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala		
725	730	735
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp		
740	745	750
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr		
755	760	765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met		
770	775	780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly		
785	790	795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu		
805	810	815
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu		
820	825	830
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys		
835	840	845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln		
850	855	860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu		
865	870	875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn		
885	890	895
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr		
900	905	910
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val		
915	920	925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys		
930	935	940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys		
945	950	955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser		
965	970	975
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys		
980	985	990
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser		
995	1000	1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile		

1010		1015		1020	
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr					
1025		1030		1035	104
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln					
	1045		1050		1055
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu					
	1060		1065		1070
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro					
	1075		1080		1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr					
	1090		1095		1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu					
1105		1110		1115	112
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile					
	1125		1130		1135
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu					
	1140		1145		1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met					
	1155		1160		1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly					
	1170		1175		1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys					
1185		1190		1195	120
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe					
	1205		1210		1215
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu					
	1220		1225		1230
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser					
	1235		1240		1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys					
	1250		1255		1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp					
1265		1270		1275	128
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn					
	1285		1290		1295
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn					
	1300		1305		1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser					
	1315		1320		1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn					
	1330		1335		1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp					
1345		1350		1355	136
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly					
	1365		1370		1375
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val					
	1380		1385		1390
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln					
	1395		1400		1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser					
	1410		1415		1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys					

1425	1430	1435	144
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu			
	1445	1450	1455
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys			
	1460	1465	1470
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His			
	1475	1480	1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val			
	1490	1495	1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr			
1505	1510	1515	152
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys			
	1525	1530	1535
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly			
	1540	1545	1550
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys			
	1555	1560	1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu			
1570	1575	1580	
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn			
1585	1590	1595	160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu			
	1605	1610	1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser			
	1620	1625	1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala			
	1635	1640	1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile			
1650	1655	1660	
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser			
1665	1670	1675	168
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly			
	1685	1690	1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly			
	1700	1705	1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp			
	1715	1720	1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser			
1730	1735	1740	
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser			
1745	1750	1755	176
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu			
	1765	1770	1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser			
	1780	1785	1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile			
	1795	1800	1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn			
1810	1815	1820	
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly			
1825	1830	1835	184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His			

	1845		1850		1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys					
	1860		1865		1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys					
	1875		1880		1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu					
	1890		1895		1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val					
1905	1910		1915		192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met					
	1925		1930		1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu					
	1940		1945		1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser					
	1955		1960		1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys					
	1970		1975		1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe					
1985	1990		1995		200
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe					
	2005		2010		2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala					
	2020		2025		2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn					
	2035		2040		2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys					
	2050		2055		2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu					
2065	2070		2075		208
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro					
	2085		2090		2095
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg					
	2100		2105		2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys					
	2115		2120		2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu					
	2130		2135		2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln					
2145	2150		2155		216
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn					
	2165		2170		2175
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met					
	2180		2185		2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn					
	2195		2200		2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu					
	2210		2215		2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu					
2225	2230		2235		224
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys					
	2245		2250		2255
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg					

2260	2265	2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn		
2275	2280	2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu		
2290	2295	2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu		
2305	2310	2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg		
2325	2330	2335
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro		
2340	2345	2350
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu		
2355	2360	2365
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln		
2370	2375	2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly		
2385	2390	2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe		
2405	2410	2415
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg		
2420	2425	2430
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys		
2435	2440	2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln		
2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu		
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		
2485	2490	2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		
2500	2505	2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		
2515	2520	2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		
2530	2535	2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		
2565	2570	2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		
2580	2585	2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		
2595	2600	2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		
2610	2615	2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		
2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		
2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		

2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		
2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		
2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		
2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		
2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		
2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		
2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		
2820	2825	2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		
2835	2840	2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		
2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		
2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg		
2885	2890	2895
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala		
2900	2905	2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala		
2915	2920	2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile		
2930	2935	2940
Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln		
2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser		
2965	2970	2975
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro		
2980	2985	2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile		
2995	3000	3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn		
3010	3015	3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val		
3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His		
3045	3050	3055
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val		
3060	3065	3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala		
3075	3080	3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys		

3090	3095	3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile		
3105	3110	3115 312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu		
	3125	3130 3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu		
	3140	3145 3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn		
	3155	3160 3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu		
	3170	3175 3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser		
3185	3190	3195 320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu		
	3205	3210 3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu		
	3220	3225 3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met		
	3235	3240 3245
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn		
	3250	3255 3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro		
3265	3270	3275 328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys		
	3285	3290 3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile		
	3300	3305 3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe		
	3315	3320 3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu		
	3330	3335 3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys		
3345	3350	3355 336
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser		
	3365	3370 3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys		
	3380	3385 3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys		
	3395	3400 3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile		
3410	3415	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGTTTTAC CTCAGTCACA

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCTTTAAC TGTTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 3RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...36
- (D) OTHER INFORMATION: 7R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 8F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 8FIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 8RIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTGTTAGC AATTCAAC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATAATATA AATTATATGG CTTA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGTAR CTGAAGTGA ACCAAATGAT AC

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

44

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(ii) MOLECULE TYPE: Genomic DNA

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGACAGAGGT ACCTGAATC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACCTT

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

37

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGAAGCAAA ATGTAATAAG GA

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTTAAAGC ACATACATCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCTAGAGGCA AAGAATCATA C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAAGATTATT CCTTTCATTA GC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11DF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AACCAAAACA CAAATCTAAG AG

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCATTTTAA TATGCTGCTT TAC

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTTTTATAT GGAGACACAG G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTATTTACAA TTTCAACACA AGC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTTGGTCT TTCTTATGTC AG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...35

(D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA

35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(A) NAME/KEY: other

(B) LOCATION: 1...35

(D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...22

(D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACAAAATAC TGAAAGAAAG TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCACCACAG TCTCAATAG

19

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATCAAATAT TCCTTCTCTA AG

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGTAACACGA CGGCCAGTGA AAATTCAGCC TTAGC

35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT

35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11OF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11OR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGAAGATATT TGC GTT GAGG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCAGCAAAA ACCTTATGTG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACGAAAATTA TGGCAGGTTG T

21

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTTGTCTTGC GTTTTGTAAT G

21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTCATAAG TCAGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCAAATTCCT CTAACACTCC

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

37

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11TF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA

39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...42

(D) OTHER INFORMATION: 12F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA

42

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 12R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA

40

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 13-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAACATTTAA GCATCCGTTA C

21

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...28
- (D) OTHER INFORMATION: 13-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACGAGACT TTTCTCATAC TGTATTAG

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCTTTTGTCT GTTTTCCTCC AA

22

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 15-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 15FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

38

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTGGTTTGT TATAATTGTT TTTA

24

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCAAC TTTTT AGTTCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTCAGTATCA TCCTATGTG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 17AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGAAACCTTA ACCCATACTG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 18FUT/M13-AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC

39

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 18R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG

38

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...41

(D) OTHER INFORMATION: 19F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC

39

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 20F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTAACACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 20R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGTAAAACGA CGGCCAGTGG GTGTTTATG CTTGGTTCT

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACCACACCC TTAAGATGA

19

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...16
- (D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...17
- (D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TGCCAACTGG TAGCTCC

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE  
(A) NAME/KEY: other  
(B) LOCATION: 1...38  
(D) OTHER INFORMATION: 24R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE  
(A) NAME/KEY: other  
(B) LOCATION: 1...20  
(D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCTTTCGCCA AATTCAGCTA

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE  
(A) NAME/KEY: other  
(B) LOCATION: 1...20  
(D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCACTGAT ACTGGTTTTTG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TATACTTACA GGAGCCACAT

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGTGTGTAA TATTTGCG

18

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGGAAACAG CTATGACGGC AAGTTCCTCG TCAGCTATTG

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...1158
- (D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 102...602
- (D) OTHER INFORMATION: M at positions 102 or 351 = A or C;  
R at position 602 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60  
AAGTAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120  
TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180  
GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240  
AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTTG 300

```

TATCTGAAGT GGAACCAAAT GATACTGATC CATTAGATTC AAATGTAGCA MATCAGAAGC 360
CCTTTGAGAG TGGAAGTGAC AAAATCTCCA AGGAAGTTGT ACCGTCTTTG GCCTGTGAAT 420
GGTCTCAACT AACCCTTTCA GGTCTAAATG GAGCCCAGAT GGAGAAAATA CCCCTATTGC 480
ATATTTCTTC ATGTGACCAA AATATTTTCAG AAAAAGACCT ATTAGACACA GAGAACAAAA 540
GAAAGAAAGA TTTTCTTACT TCAGAGAATT CTTTGCCACG TATTTCTAGC CTACCAAAAT 600
CRGAGAAGCC ATTAAATGAG GAAACAGTGG TAAATAAGAG AGATGAAGAG CAGCATCTTG 660
AATCTCATAC AGACTGCATT CTTGCAGTAA AGCAGGCAAT ATCTGGAAC TCTCCAGTGG 720
CTTCTTCATT TCAGGGTATC AAAAAGTCTA TATTCAGAAT AAGAGAATCA CCTAAAGAGA 780
CTTTCAATGC AAGTTTTTCA GGTCATATGA CTGATCCAAA CTTTAAAAAA GAACTGAAG 840
CCTCTGAAAG TGGACTGGAA ATACATACTG TTTGCTCACA GAAGGAGGAC TCCTTATGTC 900
CAAATTTAAT TGATAATGGA AGCTGGCCAG CCACCACCAC ACAGAATTCT GTAGCTTTGA 960
AGAATGCAGG TTTAATATCC ACTTTGAAAA AGAAAACAAA TAAGTTTATT TATGCTATAC 1020
ATGATGAAAC ATTTTATAAA GGAAAAAAA TACCGAAAGA CCAAAAATCA GAACTAATTA 1080
ACTGTTTACG CCAGTTTGAA GCAAATGCTT TTGAAGCACC ACTTACATTT GCAAATGCTG 1140
ATTCAGGTAC CTCTGTCT
1158

```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...4987
- (D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 339...1917
- (D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T; R at positions 790, 1081 or 1506 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

TTTGTGTTTT TATGTTTtagg TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60
GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAAATCT GAGGAAATGT 120
TCTAGAAATG AAACATGTTT TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180
GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240
TGCTTGCAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300
GAAGAGGTCT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360
ACTGACTTTC AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420
TTAACTCCTA CTTCCTAAGGA TGTCTGTGCA AACCTAGTCA TGATTCTAG AGGCAAAGAA 480
TCATACAAAA TGTCAGACAA GCTCAAAGGT AACCAATTAT AATCTGATGT TGAATTAACC 540
AAAAATATTC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAAAAC 600
GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660
TTCAACCAAA ACACAAATCT AAGAGTAATC CAAAAAATC AAGAAGAAAC TACTTCAATT 720
TCAAAAATAA CTGTCAATCC AGACTCTGAA GAACTTTTCT CAGACAATGA GAATAATTTT 780

```

GTCTTCCAAR	TAGCTAATGA	AAGGAATAAT	CTTGCTTTAG	GAAATACTAA	GGAAC TTCAT	840
GAAACAGACT	TGACTTGTGT	AAACGAACCC	ATTTTCAAGA	ACTCTACCAT	GGTTTTATAT	900
GGAGACACAG	GTGATAAACA	AGCAACCCAA	GTGTCAATTA	AAAAAGATTT	GGTTTATGTT	960
CTTGCAGAGG	AGAACAAAAA	TAGTGTAAAG	CAGCATATAA	AAATGACTCT	AGGTCAAGAT	1020
TTAAAAATCGG	ACATCTCCTT	GAATATAGAT	AAAATACCAG	AAAAAAATAA	TGATTACATG	1080
RACAAATGGG	CAGGACTCTT	AGGTCCAATT	TCAAATCACA	GTTTTGGAGG	TAGCTTCAGA	1140
ACAGCTTCAA	ATAAGGAAAT	CAAGCTCTCT	GAACATAACA	TTAAGAAGAG	CAAAATGTTT	1200
TTCAAAGATA	TTGAAGAACA	ATATCCTACT	AGTTTAGCTT	GTGTTGAAAT	TGTAAATACC	1260
TTGGCATTAG	ATAATCAAAA	GAAACTGAGC	AAGCCTCAGT	CAATTAATAC	TGTATCTGCA	1320
CATTTACAGA	GTAGTGTAGT	TGTTTCTGAT	TGTAAAAATA	GTCATATAAC	CCCTCAGATG	1380
TTATTTTCCA	AGCAGGATTT	TAATTCAAAC	CATAATTTAA	CACCTAGCCA	AAAGGCAGAA	1440
ATTACAGAAC	TTTCTACTAT	ATTAGAAGAA	TCAGGAAGTC	AGTTTGAATT	TACTCAGTTT	1500
AGAAARCCAA	GCTACATATT	GCAGAAGAGT	ACATTTGAAG	TGCCGTGAAA	CCAGATGACT	1560
ATCTTAAAGA	CCACTTCTGA	GGAATGCAGA	GATGCTGATC	TTCATGTCAT	AATGAATGCC	1620
CCATCGATTG	GTCAAGTAGA	CAGCAGCAAG	CAATTTGAAG	GTACAGTTGA	AATTTAAACGG	1680
AAGTTTGTCTG	GCCTGTTGAA	AAATGACTGT	AACAAAAGTG	CTTCTGGTTA	TTTAAACAGAT	1740
GAAAATGAAG	TGGGGTTTTAG	GGGCTTTTAT	TCTGCTCATG	GCACAAAAC	GAATGTTTCT	1800
ACTGAAGCTC	TGCAAAAAGC	TGTGAACTG	TTTAGTGATA	TTGAGAATAT	TAGTGAGGAA	1860
ACTTCTGCAG	AGGTACATCC	AATAAGTTTA	TCTTCAAGTA	AATGTCATGA	TTCTGTYGTT	1920
TCAATGTTTTA	AGATAGAAAA	TCATAATGAT	AAAACGTGTA	GTGAAAAAAA	TAATAAATGC	1980
CAACTGTATAT	TACAAAAATA	TATTGAAATG	ACTACTGGCA	CTTTTGTGTA	AGAAATTACT	2040
GAAAATTACA	AGAGAAATAC	TGAAAATGAA	GATAACAAAT	ATACTGCTGC	CAGTAGAAAT	2100
TCTCATAACT	TAGAATTTGA	TGGCAGTGAT	TCAAGTAAAA	ATGATACTGT	TTGTATTCAT	2160
AAAGATGAAA	CGGACTTGCT	ATTTACTGAT	CAGCACAACA	TATGCTTTAA	ATTATCTGGC	2220
CAGTTTATGA	AGGAGGGAAA	CACTCAGATT	AAAGAAGATT	TGTCAGATTT	AACTTTTTTG	2280
GAAGTTGCGA	AAGCTCAAGA	AGCATGTCAT	GGTAATACTT	CAAATAAAGA	ACAGTTAACT	2340
GCTACTAAAA	CGGAGCAAAA	TATAAAAGAT	TTTGAGACTT	CTGATACATT	TTTTTCAGACT	2400
GCAAGTGGGA	AAAATATTAG	TGTCGCCAAA	GAGTCATTTA	ATAAAATTGT	AAATTTCTTT	2460
GATCAGAAAC	CAGAAGAATT	GCATAACTTT	TCCTTAAATT	CTGAATTACA	TTCTGACATA	2520
AGAAAGAACA	AAATGGACAT	TCTAAGTTAT	GAGGAAACAG	ACATAGTTAA	ACACAAAATA	2580
CTGAAAGAAA	GTGTCCCGAT	TGGTACTGGA	AATCAACTAG	TGACCTTCCA	GGGACAACCC	2640
GAACGTGATG	AAAAGATCAA	AGAACCCTACT	CTGTTGGGTT	TTCATACAGC	TAGCGGGAAA	2700
AAAGTTAAAA	TTGCAAAGGA	ATCTTTGGAC	AAAGTGAAAA	ACC'TTT'TTGA	TGAAAAAGAG	2760
CAAGGTACTA	GTGAAATCAC	CAGTTT'TTAGC	CATCAATGGG	CAAAGACCCT	AAAGTACAGA	2820
GAGGCC'TGTA	AAGACCTTGA	ATTAGCATGT	GAGACCATTG	AGATCACAGC	TGCCCCAAAG	2880
TGTAAAGAAA	TGCAGAATTC	TCTCAATAAT	GATAAAAACC	TTGTTTCTAT	TGAGACTGTG	2940
GTGCCACCTA	AGCTCTTAA	TGATAATTTA	TGTAGACAAA	CTGAAAATCT	CAAAACATCA	3000
AAAAGTATCT	TTTTGAAAGT	TAAAGTACAT	GAAAATGTAG	AAAAAGAAAC	AGCAAAAAGT	3060
CCTGCAACTT	GTTACACAAA	TCAGTCCCCT	TATTCAGTCA	TTGAAAATTC	AGCCTTAGCT	3120
TTTTACACAA	GTTGTAGTAG	AAAAACTTCT	GTGAGTCAGA	CTTCATTACT	TGAAGCAAAA	3180
AAATGGCTTA	GAGAAGGAAT	ATTTGATGGT	CAACCAGAAA	GAATAAATAC	TGCAGATTAT	3240
GTAGGAAATT	ATTTGTATGA	AAATAATTCA	AACAGTACTA	TAGCTGAAAA	TGACAAAAAT	3300
CATCTCTCCG	AAAAACAAGA	TACTTATTTA	AGTAACAGTA	GCATGTCTAA	CAGCTAT'TCC	3360
TACCAT'TCTG	ATGAGGTATA	TAATGATTCA	GGATATCTCT	CAAAAAATAA	ACTTGAT'TCT	3420
GGTATTGAGC	CAGTATTGAA	GAATGTTGAA	GATCAAAAAA	ACACTAGTTT	TTCCAAAGTA	3480
ATATCCAATG	TAAAAGATGC	AAATGCATAC	CCACAAACTG	TAAATGAAGA	TATTTGCGTT	3540
GAGGAACTTG	TGACTAGCTC	TTCAACCCTGC	AAAAATAAAA	ATGCAGCCAT	TAAATTGTCC	3600
ATATCTAATA	GTAATAATTT	TGAGGTAGGG	CCACCTGCAT	TTAGGATAGC	CAGTGGTAAA	3660
ATCGTTTGTG	TTTCACATGA	AACAATTAAA	AAAGTGAAAG	ACATATTTAC	AGACAGTTTC	3720
AGTAAAGTAA	TTAAGGAAAA	CAACGAGAAT	AAATCAAAAA	TTTGCCAAAC	GAAAATTATG	3780
GCAGGT'TGTT	ACGAGGCATT	GGATGATTCA	GAGGATATTC	TTCATAACTC	TCTAGATAAT	3840
GATGAATGTA	GCACGCATTC	ACATAAGGTT	TTTGCTGACA	TTCAGAGTGA	AGAAATTTTA	3900

```

CAACATAACC AAAATATGTC TGGATTGGAG AAAGTTTCTA AAATATCACC TTGTGATGTT 3960
AGTTTGGAAA CTTCAGATAT ATGTAAATGT AGTATAGGGA AGCTTCATAA GTCAGTCTCA 4020
TCTGCAAATA CTTGTGGGAT TTTTAGCACA GCAAGTGGAA AATCTGTCCA GGTATCAGAT 4080
GCTTCATTAC AAAACGCAAG ACAAGTGTTC TCTGAAATAG AAGATAGTAC CAAGCAAGTC 4140
TTTTCCAAAG TATTGTTTAA AAGTAACGAA CATTAGACC AGCTCACAAG AGAAGAAAAT 4200
ACTGCTATAC GTACTCCAGA ACATTTAATA TCCCAAAAAG GCTTTTCATA TAATGTGGTA 4260
AATTCATCTG CTTTCTCTGG ATTTAGTACA GCAAGTGGAA AGCAAGTTTC CATTTTAGAA 4320
AGTTCCTTAC ACAAAGTTAA GGGAGTGTTA GAGGAATTTG ATTTAATCAG AACTGAGCAT 4380
AGTCTTCACT ATTCACCTAC GTCTAGACAA AATGTATCAA AAATACTTCC TCGTGTGAT 4440
AAGAGAAACC CAGAGCACTG TGTAAACTCA GAAATGGAAA AAACCTGCAG TAAAGAATTT 4500
AAATTATCAA ATAACTTAAA TGTTGAAGGT GGTTCCTCAG AAAATAATCA CTCTATTAAA 4560
GTTTCTCCAT ATCTCTCTCA ATTTCAACAA GACAAACAAC AGTTGGTATT AGGAACCAA 4620
GTCTCACTTG TTGAGAACAT TCATGTTTTG GGAAGAAGAAC AGGCTTCACC TAAAAACGTA 4680
AAAATGGAAA TTGGTAAAAC TGAAACTTTT TCTGATGTTT CTGTGAAAAC AAATATAGAA 4740
GTTTGTCTTA CTTACTCCAA AGATTAGAA AACTACTTTG AAACAGAAGC AGTAGAAAT 4800
GCTAAAGCTT TTATGGAAGA TGATGAAC TGATGAAC TGATGAAC TGATGAAC TGATGAAC 4860
CATTCCTCTT TTACATGTCC CGAAAATGAG GAAATGGTTT TGTCAAATTC AAGAATTGGA 4920
AAAAGAAGAG GAGAGCCCCT TATCTTAGTG GGTAAAGTGT CATTTTTACC TTTCGTGTTG 4980
CCAATCA 4987

```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...468
- (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 248
- (D) OTHER INFORMATION: R at position 248 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

CCCCATTGCA GCACAACCTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
GGTCAAGAAT TTCTGTCTAA ATCTCATTTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCACC TTTTAAACT 240
AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAAGTTGGA GGAAAACAGA 300
CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAT 360
GAGATTTCATC AGTTTAAACAA AAACAACTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
TGTGAAGAAG AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT 468

```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...255
- (D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 127
- (D) OTHER INFORMATION: R at position 127 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
TTTTTATTC C AATATCTTAA ATGGTCACAG GGTATTTC A GTGAAGAGCA GTTAAGAGCC 60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT 120
AGGAAGRCCA TGGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTCACAACC 180
GTGTGGAAGT TGCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA 240
AATGCTTTGT TTTTA                                     255
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...135
- (D) OTHER INFORMATION: Exon 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
TAAGTGCATT TTGGTCTTCT GTTTTCGAGA CTTATTTACC AAGCATTGGA GGAATATCGT 60
AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC 120
GCTGCAACAA AGCAGGTATT GACAAATTTT ATATAAC                                     157
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 21...269

(D) OTHER INFORMATION: Exon 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
GGGATTTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTTG AAGAACTTTC 60
TTCAGAAGCT CCACCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACCTCCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180
AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 26...134

(D) OTHER INFORMATION: Exon 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
TCACTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60
CGCACAGTGA AAAC TAAAAT GGATCAAGCA GATGATGTTT CCTGTCCACT TCTAAATTCT 120
TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...71

(D) OTHER INFORMATION: Exon 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTAACAATTT TCCCCTTTTT TTACCCCCAG TGGTATGTGG GAGTTTGTTC CATACACCAA 60  
AGTTTGTGAA GGTAAATATT 80

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 51...165
- (D) OTHER INFORMATION: Exon 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TAATGATCAG GGCATTTCTA TAAAAAATAA ACTATTTTCT TTCCTCCCAG GGTGTCGAGA 60  
CACCAAAACA TATTTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 120  
GTTCTTTAGC TACACCACCC ACCCTTAGTT CTA CTGTGCT CATAGGTAAT AATA 174

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 14...63
- (D) OTHER INFORMATION: Exon 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTTCCCTCA TGATACTACT 60  
GCTGTAAGTA AATATGACAT TGATTAGACT 90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 20...131
- (D) OTHER INFORMATION: Exon 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TAAACTATAA TTTTTCGAGA ATGTGAAAAG CTATTTTTC AATCATGATG AAAGTCTGAA 60
GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120
TGCAAGTCAT GGTAAGTCCT CT 142
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...124
- (D) OTHER INFORMATION: Exon 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60
GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120
GATGGTAAAA TTAGCTTTTT ATTTATA 147
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...100
- (D) OTHER INFORMATION: Exon 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60
ATCATGTTTC TTTAGAGCCG ATTACCTGTG TACCCTTTTCG GTAAGACATG TTAAATTTT 120
TCTAA 125
```

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 199 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 13...183
  - (D) OTHER INFORMATION: Exon 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

TTATTTGTTT AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTAT AATCACTATA GATGGATCAT ATGGAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT                                     199

```

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 19...373
  - (D) OTHER INFORMATION: Exon 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

TTTTGTTTTT ACTTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60
AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACACTT GTTCTCTGTG TTTCTGACAT 120
AATTTCATTG AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180
CCAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240
TCCTCCCCCT TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300
TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360
TCTTATGTTA AAGGTAAATT                                     380

```

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 30...185
- (D) OTHER INFORMATION: Exon 19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60
GGTATACCAA ACTTGGATTCTTTCTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120
TTTTCACTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180
TACAGGTATG ATGTATTCTT GAAACTTA                                     208
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 28...172
- (D) OTHER INFORMATION: Exon 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
TTTCGCAATG AAAGAGAGGA AGAAAAGGAA GCAGCAAAAT ATGTGGAGGC CCAACAAAAG 120
AGACTAGAAG CCTTATTCAC TAAAATTTCAG GAGGAATTTG AAGAACATGA AGGTAAAATT 180
AGTTATATGG TACACATTGT TATTTCT                                     206
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 36...157
- (D) OTHER INFORMATION: Exon 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
AGTTTAGTGA ATTAATAATC CTTTGTGTTT CTTAGAAAAC ACAACAAAAC CATATTTTACC 60
ATCACGTGCA CTAACAAGAC AGCAAGTTCTG TGCTTTGCAA GATGGTGCAG AGCTTTTATGA 120
AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180
```

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 12...175
- (D) OTHER INFORMATION: Exon 23

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
AGAAGGAAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAAAGCTCAG TATCAACAAC TACCGGTACA 180
AACCTTTCAT TGTAATTTT 200
```

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 25...163
- (D) OTHER INFORMATION: Exon 24

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTTTGT TTTGTTTCT GTAGGTTTCA GATGAAATTT TATTTTCAGAT TTACCAGCCA 60
CGGGAGCCCC TTCACTTCAG CAAATTTTTA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
GTGGACCTAA TAGGATTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
TAATTTT TATTGATTCT TTTAAAAAAC ATTGTCT 217
```

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...275

(D) OTHER INFORMATION: Exon 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
TAACATTCTT TTCTTTTTTT TCCATTCTAG GACTTGCCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA 284
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...177

(D) OTHER INFORMATION: Exon 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
ATAAAGCAGC TTTTCCACTT ATTTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60
AACAAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCCC AACTAAAGAC 120
TGTACTTCAG GGCCGTACAC TGCTCAAATC ATTCCTGGTA CAGGAAACAA GCTTCTGGTA 180
AGTTAATGTA AACTCAAGGA ATATTATAAG 210
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 23...691

(D) OTHER INFORMATION: Exon 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
TACGTTTTCA TTTTTTTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60
```

TTTATCACTT	TGTATGGCCA	AAAGGAAGTC	TGTTTCCACA	CCTGTCTCAG	CCCAGATGAC	120
TTCAAAGTCT	TGTAAAGGGG	AGAAAGAGAT	TGATGACCAA	AAGAACTGCA	AAAAGAGAAG	180
AGCCTTGGAT	TTCTTGAGTA	GACTGCCTTT	ACCTCCACCT	GTTAGTCCCA	TTTGTACATT	240
TGTTTCTCCG	GCTGCACAGA	AGGCATTTC	GCCACCAAGG	AGTTGTGGCA	CCAAATACGA	300
AACACCCATA	AAGAAAAAAG	AACTGAATTC	TCCTCAGATG	ACTCCATTTA	AAAAATTCAA	360
TGAAATTTCT	CTTTTGGA	GTAATTCAAT	AGCTGACGAA	GAACCTGCAT	TGATAAATAC	420
CCAAGCTCTT	TTGTCTGGTT	CAACAGGAGA	AAAACAATTT	ATATCTGTCA	GTGAATCCAC	480
TAGGACTGCT	CCCACCAGTT	CAGAAGATTA	TCTCAGACTG	AAACGACGTT	GTACTACATC	540
TCTGATCAAA	GAACAGGAGA	GTTCCCAGGC	CAGTACGGAA	GAATGTGAGA	AAAATAAGCA	600
GGACACAATT	ACAATAAAA	AATATATCTA	AGCATTTGCA	AAGGCGACAA	TAAATTATTG	660
ACGCTTAACC	TTTCCAGTTT	ATAAGACTGG	A			691